```
                        GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:         January  6, 2006, 16:35:28 ; Search time 72.2917 Seconds
                                             (without alignments)
                                             30.389 Million cell updates/sec

Title:          US-10-528-928-1
Perfect score:  5
Sequence:       1 EVHHQ 5


Scoring table:  OLIGO
                Gapop 60.0 , Gapext 60.0


Searched:       2443163 seqs, 439378781 residues


Word size :     0


Total number of hits satisfying chosen parameters:      2443163


Minimum DB seq length: 0
Maximum DB seq length: 2000000000


Post-processing: Listing first 45 summaries


Database :      A_Geneseq_21:*
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                2:  geneseqp1990s:*
                3:  geneseqp2000s:*
                4:  geneseqp2001s:*
                5:  geneseqp2002s:*
                6:  geneseqp2003as:*
                7:  geneseqp2003bs:*
                8:  geneseqp2004s:*
                9:  geneseqp2005s:*


        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                SUMMARIES
                %
Result          Query
   No.   Score  Match Length DB   ID                  Description
-----------------------------------------------------------------------------
        1      5  100.0      5  2  AAW45954            Aaw45954 Amyloid b
        2      5  100.0      5  8  ADO00814            Ado00814 Human amy
        3      5  100.0      5  8  ADO43840            Ado43840 Immunogen
        4      5  100.0      5  8  ADQ37309            Adq37309 Antifibri
        5      5  100.0      6  2  AAW45948            Aaw45948 Amyloid b
        6      5  100.0      6  7  ADB75168            Adb75168 Human amy
        7      5  100.0      6  8  ADJ71470            Adj71470 N-termina
        8      5  100.0      7  2  AAW45943            Aaw45943 Amyloid b
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 9     5    100.0      7    6    AAE35433          Aae35433 Abeta pep
10     5    100.0      7    6    ADA90149          Ada90149 Anti-Abet
11     5    100.0      7    6    ADA90932          Ada90932 Solid-pha
12     5    100.0      7    6    ADA90148          Ada90148 Anti-Abet
13     5    100.0      7    6    ADA90931          Ada90931 Solid-pha
14     5    100.0      7    8    ADJ71471          Adj71471 N-termina
15     5    100.0      7    8    ADJ71458          Adj71458 N-termina
16     5    100.0      7    8    ADO00815          Ado00815 Human amy
17     5    100.0      7    8    ADO43841          Ado43841 Immunogen
18     5    100.0      7    8    ADQ37257          Adq37257 Vaccine a
19     5    100.0      7    9    ADZ08902          Adz08902 Human bet
20     5    100.0      8    2    AAW45939          Aaw45939 Amyloid b
21     5    100.0      8    8    ADJ71459          Adj71459 N-termina
22     5    100.0      8    8    ADJ71472          Adj71472 N-termina
23     5    100.0      8    8    ADJ71446          Adj71446 N-termina
24     5    100.0      9    8    ADI35864          Adi35864 Amyloid b
25     5    100.0      9    8    ADI35872          Adi35872 Amyloid b
26     5    100.0      9    8    ADI35901          Adi35901 Amyloid b
27     5    100.0      9    8    ADI35916          Adi35916 Amyloid b
28     5    100.0      9    8    ADI35952          Adi35952 Amyloid b
29     5    100.0      9    8    ADI35954          Adi35954 Amyloid b
30     5    100.0      9    8    ADI35974          Adi35974 Amyloid b
31     5    100.0      9    8    ADI35896          Adi35896 Amyloid b
32     5    100.0      9    8    ADI35930          Adi35930 Amyloid b
33     5    100.0      9    8    ADI35996          Adi35996 Amyloid b
34     5    100.0      9    8    ADI36002          Adi36002 Amyloid b
35     5    100.0      9    8    ADI35902          Adi35902 Amyloid b
36     5    100.0      9    8    ADI35905          Adi35905 Amyloid b
37     5    100.0      9    8    ADI35915          Adi35915 Amyloid b
38     5    100.0      9    8    ADI35969          Adi35969 Amyloid b
39     5    100.0      9    8    ADI35984          Adi35984 Amyloid b
40     5    100.0      9    8    ADI35851          Adi35851 Amyloid b
41     5    100.0      9    8    ADI35993          Adi35993 Amyloid b
42     5    100.0      9    8    ADI36007          Adi36007 Amyloid b
43     5    100.0      9    8    ADI35897          Adi35897 Amyloid b
44     5    100.0      9    8    ADI35933          Adi35933 Amyloid b
45     5    100.0      9    8    ADI35934          Adi35934 Amyloid b
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ALIGNMENTS

RESULT 1
AAW45954
ID   AAW45954 standard; peptide; 5 AA.
XX
AC   AAW45954;
XX
DT   25-MAR-2003 (revised)
DT   30-JUN-1998 (first entry)
XX
DE   Amyloid beta peptide fragment.
XX
KW   Amyloid beta peptide; Alzheimer's disease; polymerisation; aggregation;
KW   positron emission tomography; PET; Down's syndrome; amyloidosis.
XX
OS   Homo sapiens.

Search completed: January 6, 2006, 16:51:40
Job time : 73.2917 secs

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OM protein - protein search, using sw model

Run on: January 6, 2006, 16:45:19 ; Search time 20.625 Seconds
                                              (without alignments)
                                              20.043 Million cell updates/sec

Title: US-10-528-928-1
Perfect score: 5
Sequence: 1 EVHHQ 5

Scoring table: OLIGO
                  Gapop 60.0 , Gapext 60.0

Searched: 572060 seqs, 82675679 residues

Word size :   0

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :   Issued_Patents_AA:*
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                  3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
                  4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                  5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
                  6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

            Pred. No. is the number of results predicted by chance to have a
            score greater than or equal to the score of the result being printed,
            and is derived by analysis of the total score distribution.

                                    SUMMARIES
                    %
Result   Query
   No.   Score Match Length DB ID   Description
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     1   5 100.0   5 2 US-09-095-106A-23   Sequence 23, Appl
     2   5 100.0   6 2 US-09-095-106A-18   Sequence 18, Appl
     3   5 100.0   7 2 US-09-095-106A-14   Sequence 14, Appl
     4   5 100.0   8 2 US-09-095-106A-10   Sequence 10, Appl
     5   5 100.0   9 2 US-09-095-106A-7   Sequence 7, Appli
     6   5 100.0   10 2 US-09-095-106A-2   Sequence 2, Appli
     7   5 100.0   10 2 US-09-724-961-14   Sequence 14, Appl
     8   5 100.0   10 2 US-09-724-961-15   Sequence 15, Appl

9	5	100.0	10	2	US-09-724-961-16	Sequence 16, Appl
10	5	100.0	10	2	US-09-724-961-17	Sequence 17, Appl
11	5	100.0	10	2	US-09-724-961-18	Sequence 18, Appl
12	5	100.0	10	2	US-09-724-961-19	Sequence 19, Appl
13	5	100.0	10	2	US-09-580-018-14	Sequence 14, Appl
14	5	100.0	10	2	US-09-580-018-15	Sequence 15, Appl
15	5	100.0	10	2	US-09-580-018-16	Sequence 16, Appl
16	5	100.0	10	2	US-09-580-018-17	Sequence 17, Appl
17	5	100.0	10	2	US-09-580-018-18	Sequence 18, Appl
18	5	100.0	10	2	US-09-580-018-19	Sequence 19, Appl
19	5	100.0	10	2	US-09-724-551-14	Sequence 14, Appl
20	5	100.0	10	2	US-09-724-551-15	Sequence 15, Appl
21	5	100.0	10	2	US-09-724-551-16	Sequence 16, Appl
22	5	100.0	10	2	US-09-724-551-17	Sequence 17, Appl
23	5	100.0	10	2	US-09-724-551-18	Sequence 18, Appl
24	5	100.0	10	2	US-09-724-551-19	Sequence 19, Appl
25	5	100.0	10	2	US-09-724-940-14	Sequence 14, Appl
26	5	100.0	10	2	US-09-724-940-15	Sequence 15, Appl
27	5	100.0	10	2	US-09-724-940-16	Sequence 16, Appl
28	5	100.0	10	2	US-09-724-940-17	Sequence 17, Appl
29	5	100.0	10	2	US-09-724-940-18	Sequence 18, Appl
30	5	100.0	10	2	US-09-724-940-19	Sequence 19, Appl
31	5	100.0	11	2	US-08-766-596A-68	Sequence 68, Appl
32	5	100.0	11	2	US-09-623-548A-957	Sequence 957, App
33	5	100.0	11	2	US-09-623-548A-963	Sequence 963, App
34	5	100.0	11	2	US-09-623-548A-990	Sequence 990, App
35	5	100.0	11	2	US-09-657-276-957	Sequence 957, App
36	5	100.0	11	2	US-09-657-276-963	Sequence 963, App
37	5	100.0	11	2	US-09-657-276-990	Sequence 990, App
38	5	100.0	15	1	US-08-609-090-1	Sequence 1, Appli
39	5	100.0	15	1	US-08-612-785B-4	Sequence 4, Appli
40	5	100.0	15	1	US-08-612-785B-37	Sequence 37, Appl
41	5	100.0	15	2	US-08-617-267C-4	Sequence 4, Appli
42	5	100.0	16	1	US-08-302-808-10	Sequence 10, Appl
43	5	100.0	16	1	US-08-659-984A-20	Sequence 20, Appl
44	5	100.0	16	1	US-08-986-948-10	Sequence 10, Appl
45	5	100.0	16	2	US-08-660-531-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1
US-09-095-106A-23
; Sequence 23, Application US/09095106A
; Patent No. 6331440
; GENERAL INFORMATION:
; APPLICANT: NORDSTEDT, Christer
; APPLICANT: NASLUND, Jan
; APPLICANT: THYBERG, Johan
; APPLICANT: TJERNBERG, Lars O.
; APPLICANT: TERENIUS, Lars
; TITLE OF INVENTION: PEPTIDE BINDING THE KLVFF-SEQUENCE OF AMYLOID-BETA
; FILE REFERENCE: 000500-124
; CURRENT APPLICATION NUMBER: US/09/095,106A
; CURRENT FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: US 60/009,386

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Qy        1  EVHHQ  5
             |||||
Db        4  EVHHQ  8
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Search completed: January 6, 2006, 17:01:10
Job time : 20.625 secs

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OM protein - protein search, using sw model

Run on: January 6, 2006, 16:45:55 ; Search time 45.625 Seconds
                                              (without alignments)
                                              45.790 Million cell updates/sec

Title: US-10-528-928-1
Perfect score: 5
Sequence: 1 EVHHQ 5

Scoring table: OLIGO
                 Gapop 60.0 , Gapext 60.0

Searched: 1867569 seqs, 417829326 residues

Word size :   0

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :   Published_Applications_AA_Main:*
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                 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
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                 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	5	100.0	5	3	US-09-850-061A-23	Sequence 23, Appl
2	5	100.0	5	4	US-10-721-774-23	Sequence 23, Appl
3	5	100.0	6	3	US-09-850-061A-18	Sequence 18, Appl
4	5	100.0	6	4	US-10-084-380A-9	Sequence 9, Appli
5	5	100.0	6	4	US-10-721-774-18	Sequence 18, Appl
6	5	100.0	6	5	US-10-625-854-133	Sequence 133, App
7	5	100.0	7	3	US-09-867-847-6	Sequence 6, Appli
8	5	100.0	7	3	US-09-850-061A-14	Sequence 14, Appl

Search completed: January 6, 2006, 17:05:00
Job time : 46.625 secs

                          GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 6, 2006, 16:51:56 ; Search time 3.125 Seconds
                                              (without alignments)
                                              13.579 Million cell updates/sec

Title: US-10-528-928-1
Perfect score: 5
Sequence: 1 EVHHQ 5

Scoring table: OLIGO
                 Gapop 60.0 , Gapext 60.0

Searched: 61072 seqs, 8486849 residues

Word size :   0

Total number of hits satisfying chosen parameters: 61072

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :   Published_Applications_AA_New:*
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                 3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
                 4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
                 5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
                 6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
                 7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
                 8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                  SUMMARIES
              %
Result   Query
  No. Score Match Length DB ID   Description
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     2   5 100.0   28 6 US-10-250-581-5   Sequence 5, Appli
     3   5 100.0   28 6 US-10-250-581-8   Sequence 8, Appli
     4   5 100.0   28 6 US-10-250-581-11   Sequence 11, Appl
     5   5 100.0   28 6 US-10-250-581-14   Sequence 14, Appl

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 6      5  100.0    28   6   US-10-250-581-17        Sequence 17, Appl
 7      5  100.0    28   6   US-10-250-581-2         Sequence 2, Appli
 8      5  100.0    28   6   US-10-250-581-5         Sequence 5, Appli
 9      5  100.0    28   6   US-10-250-581-8         Sequence 8, Appli
10      5  100.0    28   6   US-10-250-581-11        Sequence 11, Appl
11      5  100.0    28   6   US-10-250-581-14        Sequence 14, Appl
12      5  100.0    28   6   US-10-250-581-17        Sequence 17, Appl
13      5  100.0    40   6   US-10-250-581-3         Sequence 3, Appli
14      5  100.0    40   6   US-10-250-581-6         Sequence 6, Appli
15      5  100.0    40   6   US-10-250-581-9         Sequence 9, Appli
16      5  100.0    40   6   US-10-250-581-12        Sequence 12, Appl
17      5  100.0    40   6   US-10-250-581-15        Sequence 15, Appl
18      5  100.0    40   6   US-10-250-581-18        Sequence 18, Appl
19      5  100.0    40   6   US-10-250-581-3         Sequence 3, Appli
20      5  100.0    40   6   US-10-250-581-6         Sequence 6, Appli
21      5  100.0    40   6   US-10-250-581-9         Sequence 9, Appli
22      5  100.0    40   6   US-10-250-581-12        Sequence 12, Appl
23      5  100.0    40   6   US-10-250-581-15        Sequence 15, Appl
24      5  100.0    40   6   US-10-250-581-18        Sequence 18, Appl
25      5  100.0    40   7   US-11-016-706-36        Sequence 36, Appl
26      5  100.0    40   7   US-11-098-674-12        Sequence 12, Appl
27      5  100.0    42   6   US-10-923-605-1         Sequence 1, Appli
28      5  100.0    42   6   US-10-934-818-1         Sequence 1, Appli
29      5  100.0    42   6   US-10-250-581-4         Sequence 4, Appli
30      5  100.0    42   6   US-10-250-581-7         Sequence 7, Appli
31      5  100.0    42   6   US-10-250-581-10        Sequence 10, Appl
32      5  100.0    42   6   US-10-250-581-13        Sequence 13, Appl
33      5  100.0    42   6   US-10-250-581-16        Sequence 16, Appl
34      5  100.0    42   6   US-10-250-581-19        Sequence 19, Appl
35      5  100.0    42   6   US-10-250-581-4         Sequence 4, Appli
36      5  100.0    42   6   US-10-250-581-7         Sequence 7, Appli
37      5  100.0    42   6   US-10-250-581-10        Sequence 10, Appl
38      5  100.0    42   6   US-10-250-581-13        Sequence 13, Appl
39      5  100.0    42   6   US-10-250-581-16        Sequence 16, Appl
40      5  100.0    42   6   US-10-250-581-19        Sequence 19, Appl
41      5  100.0    42   7   US-11-016-706-37        Sequence 37, Appl
42      5  100.0    43   6   US-10-934-818-6         Sequence 6, Appli
43      5  100.0    43   6   US-10-250-581-1         Sequence 1, Appli
44      5  100.0    43   6   US-10-250-581-1         Sequence 1, Appli
45      5  100.0   438   6   US-10-641-678-49        Sequence 49, Appl
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ALIGNMENTS

RESULT 1
US-10-250-581-2
; Sequence 2, Application US/10250581
; Publication No. US20040116337A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Society for Promotion of Applied ...
; TITLE OF INVENTION: Soluble cyclic analogs....
; FILE REFERENCE: 16069
; CURRENT APPLICATION NUMBER: US/10/250,581
; CURRENT FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Version 2.1

Search completed: January 6, 2006, 17:05:26
Job time : 3.125 secs

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OM protein - protein search, using sw model

Run on: January 6, 2006, 16:43:17 ; Search time 13.9583 Seconds
                                            (without alignments)
                                            34.466 Million cell updates/sec

Title: US-10-528-928-1
Perfect score: 5
Sequence: 1 EVHHQ 5

Scoring table: OLIGO
                 Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size :   0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :   PIR_80:*
                 1: pir1:*
                 2: pir2:*
                 3: pir3:*
                 4: pir4:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	5	100.0	42	2	PN0512	beta-amyloid prote
2	5	100.0	57	2	A60045	Alzheimer's diseas
3	5	100.0	57	2	F60045	Alzheimer's diseas
4	5	100.0	57	2	D60045	Alzheimer's diseas
5	5	100.0	57	2	E60045	Alzheimer's diseas
6	5	100.0	57	2	G60045	Alzheimer's diseas
7	5	100.0	57	2	B60045	Alzheimer's diseas
8	5	100.0	82	2	PQ0438	Alzheimer's diseas
9	5	100.0	122	2	G98033	hypothetical prote
10	5	100.0	230	2	I39161	dystonin isoform 2

11	5	100.0	284	2	S04723	genome polyprotein
12	5	100.0	306	2	T06642	hypothetical prote
13	5	100.0	313	2	JT0960	polyprotein - pota
14	5	100.0	327	2	S11435	genome polyprotein
15	5	100.0	330	2	A26205	coat protein precu
16	5	100.0	379	2	S13556	genome polyprotein
17	5	100.0	427	2	JA0073	genome polyprotein
18	5	100.0	519	2	PC1072	nuclear inclusion
19	5	100.0	695	1	A49795	Alzheimer's diseas
20	5	100.0	747	2	JH0773	Alzheimer's diseas
21	5	100.0	770	1	QRHUA4	Alzheimer's diseas
22	5	100.0	829	2	C82361	GGDEF family prote
23	5	100.0	846	2	A60678	genome polyprotein
24	5	100.0	1555	2	JT0959	polyprotein - pota
25	5	100.0	3061	1	JN0545	genome polyprotein
26	5	100.0	3063	2	JS0166	genome polyprotein
27	4	80.0	25	2	B34461	heat shock protein
28	4	80.0	57	2	F90778	hypothetical prote
29	4	80.0	73	2	S28480	rfbP protein - Vib
30	4	80.0	78	1	TIZB1A	proteinase inhibit
31	4	80.0	78	1	TIZB1B	proteinase inhibit
32	4	80.0	81	2	E95172	hypothetical prote
33	4	80.0	81	2	E98038	hypothetical prote
34	4	80.0	94	2	B75564	hypothetical prote
35	4	80.0	94	2	F31844	spdA protein - Str
36	4	80.0	101	2	S69296	probable membrane
37	4	80.0	102	2	H75352	hypothetical prote
38	4	80.0	104	2	D95003	hypothetical prote
39	4	80.0	106	2	S59536	cold stress protei
40	4	80.0	106	2	E90196	hypothetical prote
41	4	80.0	115	2	T36957	hypothetical prote
42	4	80.0	117	2	G97875	hypothetical prote
43	4	80.0	117	2	C72691	hypothetical prote
44	4	80.0	122	2	A86900	glutamine syntheta
45	4	80.0	129	2	AF2141	hypothetical prote

ALIGNMENTS

RESULT 1
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beta-amyloid protein - guinea pig (fragment)
C;Species: Cavia porcellus (guinea pig)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: PN0512
R;Shimohigashi, Y.; Matsumoto, H.; Takano, Y.; Saito, R.; Iwata, T.; Kamiya, H.;
Ohno, M.
Biochem. Biophys. Res. Commun. 193, 624-630, 1993
A;Title: Receptor-mediated specific biological activity of a beta-amyloid
protein fragment for NK-1 substance p receptors.
A;Reference number: PN0512; MUID:93290653; PMID:7685598
A;Accession: PN0512
A;Molecule type: protein
A;Residues: 1-42 <SHI>
A;Cross-references: UNIPROT:Q7M088; UNIPARC:UPI00000315E8

Job time : 20.9583 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 6, 2006, 16:42:19 ; Search time 77.0833 Seconds
                                               (without alignments)
                                               45.764 Million cell updates/sec

Title: US-10-528-928-1
Perfect score: 5
Sequence: 1 EVHHQ 5

Scoring table: OLIGO
                  Gapop 60.0 , Gapext 60.0

Searched: 2166443 seqs, 705528306 residues

Word size :   0

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :   UniProt_05.80:*
                  1: uniprot_sprot:*
                  2: uniprot_trembl:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                SUMMARIES

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     2   5 100.0   42 2 Q56JJ6_GRAGR   Q56jj6 grampus gri
     3   5 100.0   42 2 Q56JJ7_TURTR   Q56jj7 tursiops tr
     4   5 100.0   42 2 Q7M088_CAVPO   Q7m088 cavia porce
     5   5 100.0   52 2 Q8WZ99_HUMAN   Q8wz99 homo sapien
     6   5 100.0   57 1 A4_URSMA   Q29149 u alzheimer
     7   5 100.0   58 1 A4_CANFA   Q28280 c alzheimer
     8   5 100.0   58 1 A4_RABIT   Q28748 o alzheimer
     9   5 100.0   58 1 A4_SHEEP   Q28757 o alzheimer
    10   5 100.0   59 1 A4_BOVIN   Q28053 b alzheimer
    11   5 100.0   103 2 Q59YA5_CANAL   Q59ya5 candida alb
    12   5 100.0   113 2 Q8JH58_CHESE   Q8jh58 chelydra se
    13   5 100.0   122 2 Q8CYL7_STRR6   Q8cyl7 streptococc
    14   5 100.0   138 2 Q59Y50_CANAL   Q59y50 candida alb

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15      5   100.0   138   2   Q9IZQ7_9POTV          Q9izq7 potato viru
16      5   100.0   153   2   Q4LH81_9BURK          Q4lh81 burkholderi
17      5   100.0   159   2   Q66U39_9DIPT          Q66u39 culicoides
18      5   100.0   159   2   Q66U41_9DIPT          Q66u41 culicoides
19      5   100.0   161   2   Q4HRM6_CAMUP          Q4hrm6 campylobact
20      5   100.0   182   2   Q6EX78_9POTV          Q6ex78 potato viru
21      5   100.0   182   2   Q6EX79_9POTV          Q6ex79 potato viru
22      5   100.0   182   2   Q6EX80_9POTV          Q6ex80 potato viru
23      5   100.0   182   2   Q6EX81_9POTV          Q6ex81 potato viru
24      5   100.0   219   2   Q5MIQ2_AEDAL          Q5miq2 aedes albop
25      5   100.0   256   2   Q5XNP4_AEDAE          Q5xnp4 aedes aegyp
26      5   100.0   259   2   Q7WVV6_STRPN          Q7wvv6 streptococc
27      5   100.0   283   2   Q9EAC3_9POTV          Q9eac3 potato viru
28      5   100.0   284   1   POLG_PVYYO            P11897 potato viru
29      5   100.0   290   2   Q9EAB6_9POTV          Q9eab6 potato viru
30      5   100.0   290   2   Q9EAB7_9POTV          Q9eab7 potato viru
31      5   100.0   290   2   Q9EAB8_9POTV          Q9eab8 potato viru
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33      5   100.0   290   2   Q9EAC6_9POTV          Q9eac6 potato viru
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ALIGNMENTS

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AC    Q9UC33;
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DT    01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT    01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE    Beta-amyloid peptide (Fragment).
OS    Homo sapiens (Human).
OC    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC    Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC    Homo.
OX    NCBI_TaxID=9606;
RN    [1]
RP    PROTEIN SEQUENCE.
RX    MEDLINE=93024877; PubMed=1406936; DOI=10.1038/359325a0;
RA    Seubert P., Vigo-Pelfrey C., Esch F., Lee M., Dovey H., Davis D.,
RA    Sinha S., Schlossmacher M., Whaley J., Swindlehurst C.;
RT    "Isolation and quantification of soluble Alzheimer's beta-peptide from
RT    biological fluids.";
RL    Nature 359:325-327(1992).
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OM protein - protein search, using sw model

Run on: January 6, 2006, 16:35:28 ; Search time 101.208 Seconds
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                                             30.389 Million cell updates/sec

Title: US-10-528-928-2
Perfect score: 7
Sequence: 1 EVHHQKI 7

Scoring table: OLIGO
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Searched: 2443163 seqs, 439378781 residues

Word size :   0

Total number of hits satisfying chosen parameters: 2443163

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Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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       Pred. No. is the number of results predicted by chance to have a
       score greater than or equal to the score of the result being printed,
       and is derived by analysis of the total score distribution.

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     4   6   85.7   7 2   AAW45943   Aaw45943 Amyloid b
     5   6   85.7   7 6   AAE35433   Aae35433 Abeta pep
     6   6   85.7   7 6   ADA90149   Ada90149 Anti-Abet
     7   6   85.7   7 6   ADA90932   Ada90932 Solid-pha
     8   6   85.7   7 8   ADJ71471   Adj71471 N-termina

9	6	85.7	7	8	ADQ37257	Adq37257	Vaccine a
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12	6	85.7	8	8	ADJ71459	Adj71459	N-termina
13	6	85.7	8	8	ADJ71472	Adj71472	N-termina
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15	6	85.7	9	8	ADI35872	Adi35872	Amyloid b
16	6	85.7	9	8	ADI35901	Adi35901	Amyloid b
17	6	85.7	9	8	ADI35916	Adi35916	Amyloid b
18	6	85.7	9	8	ADI35952	Adi35952	Amyloid b
19	6	85.7	9	8	ADI35954	Adi35954	Amyloid b
20	6	85.7	9	8	ADI35974	Adi35974	Amyloid b
21	6	85.7	9	8	ADI35896	Adi35896	Amyloid b
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ALIGNMENTS

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AC   ADO00815;
XX
DT   01-JUL-2004 (first entry)
XX
DE   Human amyloid beta_11 cleavage site, SEQ ID 2.
XX
KW   Neuroprotective; Nootropic; Haemostatic; Vaccine; Amyloid-beta 11;
KW   beta-amyloid-related disease; Alzheimer's disease; Abeta sectrease;
KW   cleavage site; immunogen; human.
XX
OS   Homo sapiens.

Search completed: January 6, 2006, 16:51:40
Job time : 101.208 secs

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OM protein - protein search, using sw model

Run on: January 6, 2006, 16:45:19 ; Search time 28.875 Seconds
                                               (without alignments)
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Title: US-10-528-928-2
Perfect score: 7
Sequence: 1 EVHHQKI 7

Scoring table: OLIGO
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Word size :   0

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Minimum DB seq length: 0
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         Pred. No. is the number of results predicted by chance to have a
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     3   6   85.7   8   2   US-09-095-106A-10   Sequence 10, Appl
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ALIGNMENTS

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; Sequence 18, Application US/09095106A
; Patent No. 6331440
; GENERAL INFORMATION:
; APPLICANT: NORDSTEDT, Christer
; APPLICANT: NASLUND, Jan
; APPLICANT: THYBERG, Johan
; APPLICANT: TJERNBERG, Lars O.
; APPLICANT: TERENIUS, Lars
; TITLE OF INVENTION: PEPTIDE BINDING THE KLVFF-SEQUENCE OF AMYLOID-BETA
; FILE REFERENCE: 000500-124
; CURRENT APPLICATION NUMBER: US/09/095,106A
; CURRENT FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: US 60/009,386

OM protein - protein search, using sw model

Run on: January 6, 2006, 16:45:55 ; Search time 63.875 Seconds
                                              (without alignments)
                                              45.790 Million cell updates/sec

Title: US-10-528-928-2
Perfect score: 7
Sequence: 1 EVHHQKI 7

Scoring table: OLIGO
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Searched: 1867569 seqs, 417829326 residues

Word size :   0

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Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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                  4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
                  5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
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        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

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     9   6   85.7   7   5   US-10-625-854-134   Sequence 134, App
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    13   6   85.7   8   5   US-10-625-854-135   Sequence 135, App
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ALIGNMENTS

RESULT 1
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; Sequence 18, Application US/09850061A
; Patent No. US20020094957A1
; GENERAL INFORMATION:
; APPLICANT: NORDSTEDT, Christer
; APPLICANT: NASLUND, Jan
; APPLICANT: THYBERG, Johan
; APPLICANT: TJERNBERG, Lars O.
; APPLICANT: TERENIUS, Lars
; TITLE OF INVENTION: PEPTIDE BINDING THE KLVFF-SEQUENCE OF AMYLOID-BETA
; FILE REFERENCE: 033315-002
; CURRENT APPLICATION NUMBER: US/09/850,061A
; CURRENT FILING DATE: 2001-05-08
; PRIOR APPLICATION NUMBER: US 09/095,106
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: PCT/SE96/01621
; PRIOR FILING DATE: 1996-12-09
; PRIOR APPLICATION NUMBER: SE 9504467-3
; PRIOR FILING DATE: 1995-12-12
; PRIOR APPLICATION NUMBER: US 60/009,386

Search completed: January 6, 2006, 17:05:00
Job time : 63.875 secs

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OM protein - protein search, using sw model

Run on: January 6, 2006, 16:51:56 ; Search time 4.375 Seconds
                                              (without alignments)
                                              13.579 Million cell updates/sec

Title: US-10-528-928-2
Perfect score: 7
Sequence: 1 EVHHQKI 7

Scoring table: OLIGO
                 Gapop 60.0 , Gapext 60.0

Searched: 61072 seqs, 8486849 residues

Word size :   0

Total number of hits satisfying chosen parameters: 61072

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :   Published_Applications_AA_New:*
                 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
                 2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
                 3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
                 4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
                 5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
                 6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
                 7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
                 8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES
                  %
Result   Query
   No.   Score   Match Length DB ID   Description
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     1   6   85.7   28 6   US-10-250-581-2   Sequence 2, Appli
     2   6   85.7   28 6   US-10-250-581-5   Sequence 5, Appli
     3   6   85.7   28 6   US-10-250-581-8   Sequence 8, Appli
     4   6   85.7   28 6   US-10-250-581-11   Sequence 11, Appl
     5   6   85.7   28 6   US-10-250-581-14   Sequence 14, Appl

6	6	85.7	28	6	US-10-250-581-17	Sequence 17, Appl
7	6	85.7	28	6	US-10-250-581-2	Sequence 2, Appli
8	6	85.7	28	6	US-10-250-581-5	Sequence 5, Appli
9	6	85.7	28	6	US-10-250-581-8	Sequence 8, Appli
10	6	85.7	28	6	US-10-250-581-11	Sequence 11, Appl
11	6	85.7	28	6	US-10-250-581-14	Sequence 14, Appl
12	6	85.7	28	6	US-10-250-581-17	Sequence 17, Appl
13	6	85.7	40	6	US-10-250-581-3	Sequence 3, Appli
14	6	85.7	40	6	US-10-250-581-6	Sequence 6, Appli
15	6	85.7	40	6	US-10-250-581-9	Sequence 9, Appli
16	6	85.7	40	6	US-10-250-581-12	Sequence 12, Appl
17	6	85.7	40	6	US-10-250-581-15	Sequence 15, Appl
18	6	85.7	40	6	US-10-250-581-18	Sequence 18, Appl
19	6	85.7	40	6	US-10-250-581-3	Sequence 3, Appli
20	6	85.7	40	6	US-10-250-581-6	Sequence 6, Appli
21	6	85.7	40	6	US-10-250-581-9	Sequence 9, Appli
22	6	85.7	40	6	US-10-250-581-12	Sequence 12, Appl
23	6	85.7	40	6	US-10-250-581-15	Sequence 15, Appl
24	6	85.7	40	6	US-10-250-581-18	Sequence 18, Appl
25	6	85.7	40	7	US-11-016-706-36	Sequence 36, Appl
26	6	85.7	40	7	US-11-098-674-12	Sequence 12, Appl
27	6	85.7	42	6	US-10-923-605-1	Sequence 1, Appli
28	6	85.7	42	6	US-10-934-818-1	Sequence 1, Appli
29	6	85.7	42	6	US-10-250-581-4	Sequence 4, Appli
30	6	85.7	42	6	US-10-250-581-7	Sequence 7, Appli
31	6	85.7	42	6	US-10-250-581-10	Sequence 10, Appl
32	6	85.7	42	6	US-10-250-581-13	Sequence 13, Appl
33	6	85.7	42	6	US-10-250-581-16	Sequence 16, Appl
34	6	85.7	42	6	US-10-250-581-19	Sequence 19, Appl
35	6	85.7	42	6	US-10-250-581-4	Sequence 4, Appli
36	6	85.7	42	6	US-10-250-581-7	Sequence 7, Appli
37	6	85.7	42	6	US-10-250-581-10	Sequence 10, Appl
38	6	85.7	42	6	US-10-250-581-13	Sequence 13, Appl
39	6	85.7	42	6	US-10-250-581-16	Sequence 16, Appl
40	6	85.7	42	6	US-10-250-581-19	Sequence 19, Appl
41	6	85.7	42	7	US-11-016-706-37	Sequence 37, Appl
42	6	85.7	43	6	US-10-934-818-6	Sequence 6, Appli
43	6	85.7	43	6	US-10-250-581-1	Sequence 1, Appli
44	6	85.7	43	6	US-10-250-581-1	Sequence 1, Appli
45	6	85.7	770	6	US-10-982-545-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1
US-10-250-581-2
; Sequence 2, Application US/10250581
; Publication No. US20040116337A1
; GENERAL INFORMATION:
; APPLICANT: Fraunhofer Society for Promotion of Applied ...
; TITLE OF INVENTION: Soluble cyclic analogs....
; FILE REFERENCE: 16069
; CURRENT APPLICATION NUMBER: US/10/250,581
; CURRENT FILING DATE: 2004-01-14
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Version 2.1

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Qy        1 EVHHQK 6
            ||||||
Db       11 EVHHQK 16
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Search completed: January 6, 2006, 17:05:26
Job time : 4.375 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 6, 2006, 16:43:17 ; Search time 19.5417 Seconds
                                             (without alignments)
                                             34.466 Million cell updates/sec

Title: US-10-528-928-2
Perfect score: 7
Sequence: 1 EVHHQKI 7

Scoring table: OLIGO
                 Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size :   0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :   PIR_80:*
                 1: pir1:*
                 2: pir2:*
                 3: pir3:*
                 4: pir4:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES

             %
Result   Query
  No.   Score Match Length DB ID   Description
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     1   6 85.7   42 2 PN0512   beta-amyloid prote
     2   6 85.7   57 2 A60045   Alzheimer's diseas
     3   6 85.7   57 2 F60045   Alzheimer's diseas
     4   6 85.7   57 2 D60045   Alzheimer's diseas
     5   6 85.7   57 2 E60045   Alzheimer's diseas
     6   6 85.7   57 2 G60045   Alzheimer's diseas
     7   6 85.7   57 2 B60045   Alzheimer's diseas
     8   6 85.7   82 2 PQ0438   Alzheimer's diseas
     9   6 85.7   695 1 A49795   Alzheimer's diseas
    10   6 85.7   747 2 JH0773   Alzheimer's diseas

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Best Local Similarity    100.0%;   Pred. No. 15;
  Matches    5;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;


Qy           2 VHHQK 6
               |||||
Db          53 VHHQK 57
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Search completed: January 6, 2006, 16:59:27
Job time : 20.5417 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 6, 2006, 16:42:19 ; Search time 107.917 Seconds
                                             (without alignments)
                                             45.764 Million cell updates/sec

Title: US-10-528-928-2
Perfect score: 7
Sequence: 1 EVHHQKI 7

Scoring table: OLIGO
                   Gapop 60.0 , Gapext 60.0

Searched: 2166443 seqs, 705528306 residues

Word size :   0

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :   UniProt_05.80:*
                   1: uniprot_sprot:*
                   2: uniprot_trembl:*

      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                              SUMMARIES

           %
Result   Query
   No.   Score Match Length DB   ID   Description
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      1   6   85.7   33 2   Q9UC33_HUMAN   Q9uc33 homo sapien
      2   6   85.7   42 2   Q56JJ6_GRAGR   Q56jj6 grampus gri
      3   6   85.7   42 2   Q56JJ7_TURTR   Q56jj7 tursiops tr
      4   6   85.7   42 2   Q7M088_CAVPO   Q7m088 cavia porce
      5   6   85.7   52 2   Q8WZ99_HUMAN   Q8wz99 homo sapien
      6   6   85.7   57 1   A4_URSMA   Q29149 u alzheimer
      7   6   85.7   58 1   A4_CANFA   Q28280 c alzheimer
      8   6   85.7   58 1   A4_RABIT   Q28748 o alzheimer
      9   6   85.7   58 1   A4_SHEEP   Q28757 o alzheimer
     10   6   85.7   59 1   A4_BOVIN   Q28053 b alzheimer
     11   6   85.7   113 2   Q8JH58_CHESE   Q8jh58 chelydra se
     12   6   85.7   219 2   Q5MIQ2_AEDAL   Q5miq2 aedes albop

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OM protein - protein search, using sw model

Run on: January 6, 2006, 16:35:28 ; Search time 72.2917 Seconds
                                             (without alignments)
                                             30.389 Million cell updates/sec

Title: US-10-528-928-3
Perfect score: 5
Sequence: 1 EVRHQ 5

Scoring table: OLIGO
                Gapop 60.0 , Gapext 60.0

Searched: 2443163 seqs, 439378781 residues

Word size :   0

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :   A_Geneseq_21:*
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                3: geneseqp2000s:*
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                5: geneseqp2002s:*
                6: geneseqp2003as:*
                7: geneseqp2003bs:*
                8: geneseqp2004s:*
                9: geneseqp2005s:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                    SUMMARIES
                    %
Result   Query
  No.   Score   Match Length DB   ID   Description
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      1   5 100.0   5 8 ADO00816   Ado00816 Murine am
      2   5 100.0   5 8 ADO43842   Ado43842 Immunogen
      3   5 100.0   7 8 ADO00817   Ado00817 Murine am
      4   5 100.0   7 8 ADO43843   Ado43843 Immunogen
      5   5 100.0   20 2 AAR86927   Aar86927 Phage dis
      6   5 100.0   24 9 AEB09195   Aeb09195 Human bet
      7   5 100.0   26 5 AAE25640   Aae25640 Murine PA
      8   5 100.0   26 9 AEB63601   Aeb63601 Poly(ADP-

9	5	100.0	32	2	AAW04402	Aaw04402 Mouse amy
10	5	100.0	32	2	AAW04401	Aaw04401 Mouse amy
11	5	100.0	32	2	AAW04400	Aaw04400 Mouse amy
12	5	100.0	40	4	AAB91786	Aab91786 Amyloid b
13	5	100.0	40	4	AAB91819	Aab91819 Amyloid b
14	5	100.0	40	4	AAB91792	Aab91792 Amyloid b
15	5	100.0	42	1	AAP83153	Aap83153 Lambda SM
16	5	100.0	42	2	AAR10025	Aar10025 Beta-amyl
17	5	100.0	42	2	AAR37867	Aar37867 Beta-amyl
18	5	100.0	42	2	AAR65284	Aar65284 Beta amyl
19	5	100.0	42	2	AAR88206	Aar88206 Rat A42 b
20	5	100.0	42	2	AAR99536	Aar99536 Murine be
21	5	100.0	42	4	AAB91785	Aab91785 Amyloid b
22	5	100.0	42	4	AAB91818	Aab91818 Amyloid b
23	5	100.0	42	4	AAB91791	Aab91791 Amyloid b
24	5	100.0	42	4	AAE03425	Aae03425 Mouse amy
25	5	100.0	42	9	AEA51411	Aea51411 Mouse A 1
26	5	100.0	42	9	AEA62822	Aea62822 Immunocon
27	5	100.0	48	6	ABP97920	Abp97920 Amino aci
28	5	100.0	52	6	ABP97925	Abp97925 Amino aci
29	5	100.0	54	5	ABP06767	Abp06767 Human ORF
30	5	100.0	55	4	AAE12903	Aae12903 Human bet
31	5	100.0	86	8	ADK72155	Adk72155 Antimicro
32	5	100.0	132	2	AAR65290	Aar65290 Rat beta
33	5	100.0	147	4	AAU42003	Aau42003 Propionib
34	5	100.0	147	6	ABM38522	Abm38522 Propionib
35	5	100.0	222	7	ABO77932	Abo77932 Pseudomon
36	5	100.0	226	7	ABO78088	Abo78088 Pseudomon
37	5	100.0	252	6	ABM66089	Abm66089 Propionib
38	5	100.0	304	7	ABO65439	Abo65439 Klebsiell
39	5	100.0	311	8	ADX87946	Adx87946 Plant ful
40	5	100.0	333	4	ABG30295	Abg30295 Novel hum
41	5	100.0	340	8	ADX94914	Adx94914 Plant ful
42	5	100.0	347	3	AAB42568	Aab42568 Human ORF
43	5	100.0	347	4	AAB92675	Aab92675 Human pro
44	5	100.0	347	8	ADX73361	Adx73361 Plant ful
45	5	100.0	354	6	ABU38975	Abu38975 Protein e

ALIGNMENTS

RESULT 1
ADO00816
ID   ADO00816 standard; peptide; 5 AA.
XX
AC   ADO00816;
XX
DT   01-JUL-2004 (first entry)
XX
DE   Murine amyloid beta_11 cleavage site, SEQ ID 3.
XX
KW   Neuroprotective; Nootropic; Haemostatic; Vaccine; Amyloid-beta 11;
KW   beta-amyloid-related disease; Alzheimer's disease; Abeta sectrease;
KW   cleavage site; immunogen; murine.
XX
OS   Mus sp.

Search completed: January 6, 2006, 16:51:42
Job time : 74.2917 secs

OM protein - protein search, using sw model

Run on: January 6, 2006, 16:45:19 ; Search time 20.625 Seconds
                                             (without alignments)
                                             20.043 Million cell updates/sec

Title: US-10-528-928-3
Perfect score: 5
Sequence: 1 EVRHQ 5

Scoring table: OLIGO
                 Gapop 60.0 , Gapext 60.0

Searched: 572060 seqs, 82675679 residues

Word size :   0

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :   Issued_Patents_AA:*
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                 2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
                 3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
                 4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                 5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
                 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                               SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	5	100.0	20	2	US-08-253-783-25	Sequence 25, Appl
2	5	100.0	20	4	PCT-US95-06726-25	Sequence 25, Appl
3	5	100.0	26	2	US-09-302-812-21	Sequence 21, Appl
4	5	100.0	26	2	US-09-511-477-21	Sequence 21, Appl
5	5	100.0	26	2	US-09-511-507-21	Sequence 21, Appl
6	5	100.0	26	2	US-09-973-451-21	Sequence 21, Appl
7	5	100.0	40	2	US-09-623-548A-962	Sequence 962, App
8	5	100.0	40	2	US-09-623-548A-968	Sequence 968, App

9	5	100.0	40	2	US-09-623-548A-995	Sequence 995, App
10	5	100.0	40	2	US-09-657-276-962	Sequence 962, App
11	5	100.0	40	2	US-09-657-276-968	Sequence 968, App
12	5	100.0	40	2	US-09-657-276-995	Sequence 995, App
13	5	100.0	42	1	US-08-271-162-5	Sequence 5, Appli
14	5	100.0	42	1	US-08-268-348A-2	Sequence 2, Appli
15	5	100.0	42	2	US-09-623-548A-961	Sequence 961, App
16	5	100.0	42	2	US-09-623-548A-967	Sequence 967, App
17	5	100.0	42	2	US-09-623-548A-994	Sequence 994, App
18	5	100.0	42	2	US-09-657-276-961	Sequence 961, App
19	5	100.0	42	2	US-09-657-276-967	Sequence 967, App
20	5	100.0	42	2	US-09-657-276-994	Sequence 994, App
21	5	100.0	42	4	PCT-US95-08302-5	Sequence 5, Appli
22	5	100.0	42	6	5220013-12	Patent No. 5220013
23	5	100.0	42	6	5223482-12	Patent No. 5223482
24	5	100.0	43	6	5187153-12	Patent No. 5187153
25	5	100.0	55	2	US-09-823-153-10	Sequence 10, Appl
26	5	100.0	133	1	US-08-268-348A-8	Sequence 8, Appli
27	5	100.0	140	2	US-09-270-767-37585	Sequence 37585, A
28	5	100.0	140	2	US-09-270-767-52802	Sequence 52802, A
29	5	100.0	222	2	US-09-252-991A-26678	Sequence 26678, A
30	5	100.0	226	2	US-09-252-991A-26834	Sequence 26834, A
31	5	100.0	304	2	US-09-489-039A-11956	Sequence 11956, A
32	5	100.0	422	2	US-09-252-991A-31797	Sequence 31797, A
33	5	100.0	427	2	US-09-252-991A-31877	Sequence 31877, A
34	5	100.0	539	2	US-09-252-991A-21463	Sequence 21463, A
35	5	100.0	695	2	US-09-458-481B-4	Sequence 4, Appli
36	5	100.0	695	2	US-09-458-481B-5	Sequence 5, Appli
37	5	100.0	695	2	US-09-458-481B-6	Sequence 6, Appli
38	5	100.0	752	2	US-09-489-039A-10195	Sequence 10195, A
39	5	100.0	968	2	US-09-302-812-6	Sequence 6, Appli
40	5	100.0	968	2	US-09-511-477-6	Sequence 6, Appli
41	5	100.0	968	2	US-09-511-507-6	Sequence 6, Appli
42	5	100.0	968	2	US-09-973-451-6	Sequence 6, Appli
43	4	80.0	10	2	US-09-139-762A-32	Sequence 32, Appl
44	4	80.0	10	2	US-09-139-762A-44	Sequence 44, Appl
45	4	80.0	10	2	US-09-139-762A-60	Sequence 60, Appl

ALIGNMENTS

RESULT 1
US-08-253-783-25
; Sequence 25, Application US/08253783
; Patent No. 6719972
; GENERAL INFORMATION:
;   APPLICANT: John G. Gribben, Gordon J. Freeman, Lee M. Nadler, Paul
;   TITLE OF INVENTION: Ligands for Induction of Antigen Specific
;   NUMBER OF SEQUENCES: 39
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: LAHIVE & COCKFIELD
;   STREET: 60 STATE STREET, suite 510
;   CITY: BOSTON
;   STATE: MASSACHUSETTS
;   COUNTRY: USA
;   ZIP: 02109-1875

US-09-623-548A-961

    Query Match   100.0%; Score 5; DB 2; Length 42;
    Best Local Similarity   100.0%; Pred. No. 3.2;
    Matches   5; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 EVRHQ 5
             |||||
Db   11 EVRHQ 15

Search completed: January 6, 2006, 17:01:11
Job time : 21.625 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 6, 2006, 16:45:55 ; Search time 45.625 Seconds
                                              (without alignments)
                                              45.790 Million cell updates/sec

Title: US-10-528-928-3
Perfect score: 5
Sequence: 1 EVRHQ 5

Scoring table: OLIGO
                  Gapop 60.0 , Gapext 60.0

Searched: 1867569 seqs, 417829326 residues

Word size :   0

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :   Published_Applications_AA_Main:*
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                  3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
                  4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
                  5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
                  6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	5	100.0	20	4	US-10-732-847A-25	Sequence 25, Appl
3	5	100.0	24	5	US-10-728-246-6	Sequence 6, Appli
4	5	100.0	26	3	US-09-973-451-21	Sequence 21, Appl
5	5	100.0	26	6	US-11-058-995-21	Sequence 21, Appl
6	5	100.0	40	6	US-11-066-697-962	Sequence 962, App
7	5	100.0	40	6	US-11-066-697-968	Sequence 968, App
8	5	100.0	40	6	US-11-066-697-995	Sequence 995, App

; TITLE OF INVENTION: METHODS FOR DETECTION OF ACTIVITY AND INHIBITORS THEREOF
; FILE REFERENCE: D0004
; CURRENT APPLICATION NUMBER: US/09/823,153
; CURRENT FILING DATE: 2001-07-02
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
;   LENGTH: 55
;   TYPE: PRT
;   ORGANISM: Human Beta App Fragment
US-09-823-153-10

   Query Match   100.0%; Score 5; DB 3; Length 55;
   Best Local Similarity   100.0%; Pred. No. 37;
   Matches   5; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 EVRHQ 5
             | | | | |
Db   11 EVRHQ 15

RESULT 15
US-10-713-981-10
; Sequence 10, Application US/10713981
; Publication No. US20040121411A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; APPLICANT: Roberts, Susan
; APPLICANT: Pak, Roger
; APPLICANT: Lewis, Martin
; APPLICANT: Smith, David
; APPLICANT: Hendrick, Joseph
; APPLICANT: Vinitsky, Alexander
; TITLE OF INVENTION: ISOLATION OF FUNCTIONALLY ACTIVE GAMMA-SECRETASE PROTEIN
COMPLEX AND
; TITLE OF INVENTION: METHODS FOR DETECTION OF ACTIVITY AND INHIBITORS THEREOF
; FILE REFERENCE: D0004 DIV
; CURRENT APPLICATION NUMBER: US/10/713,981
; CURRENT FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
;   LENGTH: 55
;   TYPE: PRT
;   ORGANISM: Human Beta App Fragment
US-10-713-981-10

   Query Match   100.0%; Score 5; DB 4; Length 55;
   Best Local Similarity   100.0%; Pred. No. 37;
   Matches   5; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   1 EVRHQ 5
             | | | | |
Db   11 EVRHQ 15

Search completed: January 6, 2006, 17:05:00
Job time : 45.625 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 6, 2006, 16:51:56 ; Search time 3.125 Seconds
                                             (without alignments)
                                             13.579 Million cell updates/sec

Title: US-10-528-928-3
Perfect score: 5
Sequence: 1 EVRHQ 5

Scoring table: OLIGO
                 Gapop 60.0 , Gapext 60.0

Searched: 61072 seqs, 8486849 residues

Word size :   0

Total number of hits satisfying chosen parameters: 61072

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :   Published_Applications_AA_New:*
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                 3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
                 4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
                 5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
                 6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
                 7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
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        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                              SUMMARIES

| | | % Query | | | | |
| Result | | | | | | |
No.	Score	Match	Length	DB	ID	Description
1	4	80.0	67	6	US-10-467-657-8570	Sequence 8570, Ap
2	4	80.0	77	6	US-10-467-657-3648	Sequence 3648, Ap
3	4	80.0	89	6	US-10-467-657-9016	Sequence 9016, Ap
4	4	80.0	91	7	US-11-074-176-352	Sequence 352, App
5	4	80.0	95	7	US-11-074-176-180	Sequence 180, App
6	4	80.0	120	6	US-10-793-626-1518	Sequence 1518, Ap

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   Query Match                  80.0%;  Score 4;  DB 6;  Length 240;
   Best Local Similarity   100.0%;  Pred. No. 76;
   Matches    4;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          2 VRHQ 5
              ||||
Db         15 VRHQ 18
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RESULT 14
US-10-793-626-2310
; Sequence 2310, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2310
;   LENGTH: 250
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: synthetic
;   OTHER INFORMATION: amino acid sequence
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (250)
;   OTHER INFORMATION: variable amino acid
US-10-793-626-2310

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   Best Local Similarity   100.0%;  Pred. No. 78;
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Qy          1 EVRH 4
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Db        176 EVRH 179
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RESULT 15
US-10-118-590-36
; Sequence 36, Application US/10118590
; Publication No. US20050277761A1
; GENERAL INFORMATION:
; APPLICANT: KENNETH RHODES, MARIA BETTY, HUAI-PING LING, AND FRANK AN
; TITLE OF INVENTION: POTASSIUM CHANNEL INTERACTORS AND USES THEREFOR
; FILE REFERENCE: MNI-070
; CURRENT APPLICATION NUMBER: US/10/118,590
; CURRENT FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: US/09/298,731
; PRIOR FILING DATE: 1999-04-23
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Query Match                80.0%;   Score 4;   DB 6;   Length 256;
Best Local Similarity   100.0%;   Pred. No. 80;
Matches    4;   Conservative    0;   Mismatches    0;   Indels    0;   Gaps    0;

Qy          2 VRHQ 5
              ||||
Db         72 VRHQ 75

A;Cross-references: UNIPROT:P08592; UNIPARC:UPI000002A2FB; EMBL:X07648;
NID:g55616; PIDN:CAA30488.1; PID:g55617
R;Schubert, D.; Schroeder, R.; LaCorbiere, M.; Saitoh, T.; Cole, G.
Science 241, 223-226, 1988
A;Title: Amyloid beta protein precursor is possibly a heparan sulfate
proteoglycan core protein.
A;Reference number: A41245; MUID:88264430; PMID:2968652
A;Accession: A41245
A;Molecule type: protein
A;Residues: 18-37,'X',39-40,'X',42-44 <SCH>
A;Cross-references: UNIPARC:UPI00001777FD
A;Note: evidence for heparan sulfate attachment
R;Hesse, L.; Beher, D.; Masters, C.L.; Multhaup, G.
FEBS Lett. 349, 109-116, 1994
A;Title: The beta-A4 amyloid precursor protein binding to copper.
A;Reference number: S46251; MUID:94320627; PMID:7913895
A;Contents: annotation; copper binding sites
A;Note: rat peptides were isolated but not sequenced
R;Potempska, A.; Styles, J.; Mehta, P.; Kim, K.S.; Miller, D.L.
J. Biol. Chem. 266, 8464-8469, 1991
A;Title: Purification and tissue level of the beta-amyloid peptide precursor of
rat brain.
A;Reference number: A39820; MUID:91217087; PMID:1673681
A;Accession: A39820
A;Status: preliminary
A;Molecule type: protein
A;Residues: 18-32 <POT>
A;Cross-references: UNIPARC:UPI00001777FE
A;Experimental source: brain
C;Comment: Deposition of amyloid protein as neurofibrillary tangles and/or
plaques is characteristic of both Alzheimer's disease and Down's syndrome.
C;Superfamily: Alzheimer's disease amyloid beta protein; animal Kunitz-type
proteinase inhibitor homology
C;Keywords: alternative splicing; amyloid; glycoprotein; transmembrane protein
F;625-648/Domain: transmembrane #status predicted <TMM>

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    Best Local Similarity    100.0%;  Pred. No. 89;
    Matches     5;  Conservative  0;  Mismatches    0;  Indels    0;  Gaps    0;


Qy           1 EVRHQ 5
               |||||
Db         607 EVRHQ 611
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Search completed: January 6, 2006, 16:59:29
Job time : 15.9583 secs

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OM protein - protein search, using sw model

Run on: January 6, 2006, 16:42:19 ; Search time 77.0833 Seconds
                                            (without alignments)
                                            45.764 Million cell updates/sec

Title: US-10-528-928-3
Perfect score: 5
Sequence: 1 EVRHQ 5

Scoring table: OLIGO
                Gapop 60.0 , Gapext 60.0

Searched: 2166443 seqs, 705528306 residues

Word size :   0

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :   UniProt_05.80:*
                1: uniprot_sprot:*
                2: uniprot_trembl:*

    Pred. No. is the number of results predicted by chance to have a
    score greater than or equal to the score of the result being printed,
    and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	5	100.0	79	2	O35463_CRIGR	O35463 cricetulus
2	5	100.0	131	2	Q9NTB8_HUMAN	Q9ntb8 homo sapien
3	5	100.0	141	2	Q4Q224_LEIMA	Q4q224 leishmania
4	5	100.0	197	2	P95796_SERMA	P95796 serratia ma
5	5	100.0	200	2	Q8GWW9_ARATH	Q8gww9 arabidopsis
6	5	100.0	215	2	Q920F7_MOUSE	Q920f7 mus musculu
7	5	100.0	218	2	Q8BPV5_MOUSE	Q8bpv5 mus musculu
8	5	100.0	221	2	Q9M7C8_TARER	Q9m7c8 tagetes ere
9	5	100.0	233	1	MTGA_SHEON	Q8eb02 shewanella
10	5	100.0	237	1	PSD_NOCFA	Q5ynv8 nocardia fa
11	5	100.0	258	2	Q9EQ67_MOUSE	Q9eq67 mus musculu
12	5	100.0	259	2	Q920F8_MOUSE	Q920f8 mus musculu

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OM protein - protein search, using sw model

Run on: January 6, 2006, 16:35:28 ; Search time 101.208 Seconds
                                             (without alignments)
                                             30.389 Million cell updates/sec

Title: US-10-528-928-4
Perfect score: 7
Sequence: 1 EVRHQKL 7

Scoring table: OLIGO
                 Gapop 60.0 , Gapext 60.0

Searched: 2443163 seqs, 439378781 residues

Word size :   0

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :   A_Geneseq_21:*
                 1: geneseqp1980s:*
                 2: geneseqp1990s:*
                 3: geneseqp2000s:*
                 4: geneseqp2001s:*
                 5: geneseqp2002s:*
                 6: geneseqp2003as:*
                 7: geneseqp2003bs:*
                 8: geneseqp2004s:*
                 9: geneseqp2005s:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

                                 SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	7	100.0	7	8	ADO00817	Ado00817 Murine am
2	7	100.0	7	8	ADO43843	Ado43843 Immunogen
3	7	100.0	24	9	AEB09195	Aeb09195 Human bet
4	7	100.0	40	4	AAB91786	Aab91786 Amyloid b
5	7	100.0	40	4	AAB91819	Aab91819 Amyloid b
6	7	100.0	40	4	AAB91792	Aab91792 Amyloid b
7	7	100.0	42	1	AAP83153	Aap83153 Lambda SM
8	7	100.0	42	2	AAR10025	Aar10025 Beta-amyl

9	7	100.0	42	2	AAR37867	Aar37867 Beta-amyl
10	7	100.0	42	2	AAR65284	Aar65284 Beta amyl
11	7	100.0	42	2	AAR88206	Aar88206 Rat A42 b
12	7	100.0	42	2	AAR99536	Aar99536 Murine be
13	7	100.0	42	4	AAB91785	Aab91785 Amyloid b
14	7	100.0	42	4	AAB91818	Aab91818 Amyloid b
15	7	100.0	42	4	AAB91791	Aab91791 Amyloid b
16	7	100.0	42	4	AAE03425	Aae03425 Mouse amy
17	7	100.0	42	9	AEA51411	Aea51411 Mouse A 1
18	7	100.0	42	9	AEA62822	Aea62822 Immunocon
19	7	100.0	48	6	ABP97920	Abp97920 Amino aci
20	7	100.0	52	6	ABP97925	Abp97925 Amino aci
21	7	100.0	55	4	AAE12903	Aae12903 Human bet
22	7	100.0	132	2	AAR65290	Aar65290 Rat beta
23	7	100.0	695	4	AAE03420	Aae03420 Human amy
24	7	100.0	695	8	ADP80871	Adp80871 Mouse amy
25	7	100.0	744	8	ABO84410	Abo84410 Mouse can
26	6	85.7	32	2	AAW04402	Aaw04402 Mouse amy
27	6	85.7	32	2	AAW04401	Aaw04401 Mouse amy
28	6	85.7	32	2	AAW04400	Aaw04400 Mouse amy
29	6	85.7	1124	9	AEA20348	Aea20348 Novel hum
30	6	85.7	1243	8	ADR14793	Adr14793 Amino aci
31	6	85.7	1243	8	ADS10797	Ads10797 Human the
32	6	85.7	1257	8	ADS12051	Ads12051 Human the
33	5	71.4	5	8	ADO00816	Ado00816 Murine am
34	5	71.4	5	8	ADO43842	Ado43842 Immunogen
35	5	71.4	20	2	AAR86927	Aar86927 Phage dis
36	5	71.4	23	6	ABO12468	Abo12468 Human zin
37	5	71.4	23	6	ABO12467	Abo12467 Human zin
38	5	71.4	23	6	ABO13108	Abo13108 Mouse zin
39	5	71.4	23	6	ABO12535	Abo12535 Human zin
40	5	71.4	23	6	ABO12478	Abo12478 Human zin
41	5	71.4	23	6	ABO13319	Abo13319 Mouse zin
42	5	71.4	26	5	AAE25640	Aae25640 Murine PA
43	5	71.4	26	9	AEB63601	Aeb63601 Poly(ADP-
44	5	71.4	38	4	ABB41876	Abb41876 Peptide #
45	5	71.4	38	4	AAM35675	Aam35675 Peptide #

ALIGNMENTS

RESULT 1
ADO00817
ID   ADO00817 standard; peptide; 7 AA.
XX
AC   ADO00817;
XX
DT   01-JUL-2004 (first entry)
XX
DE   Murine amyloid beta_11 cleavage site, SEQ ID 4.
XX
KW   Neuroprotective; Nootropic; Haemostatic; Vaccine; Amyloid-beta 11;
KW   beta-amyloid-related disease; Alzheimer's disease; Abeta sectrease;
KW   cleavage site; immunogen; murine.
XX
OS   Mus sp.

Search completed: January 6, 2006, 16:51:43
Job time : 102.208 secs

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</div>

OM protein - protein search, using sw model

Run on: January 6, 2006, 16:45:19 ; Search time 28.875 Seconds
                                             (without alignments)
                                             20.043 Million cell updates/sec

Title: US-10-528-928-4
Perfect score: 7
Sequence: 1 EVRHQKL 7

Scoring table: OLIGO
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Searched: 572060 seqs, 82675679 residues

Word size :   0

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :   Issued_Patents_AA:*
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                 3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
                 4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                 5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
                 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.

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SUMMARIES

</div>

Result No.	Score	% Query Match	Length	DB	ID	Description
1	7	100.0	40	2	US-09-623-548A-962	Sequence 962, App
2	7	100.0	40	2	US-09-623-548A-968	Sequence 968, App
3	7	100.0	40	2	US-09-623-548A-995	Sequence 995, App
4	7	100.0	40	2	US-09-657-276-962	Sequence 962, App
5	7	100.0	40	2	US-09-657-276-968	Sequence 968, App
6	7	100.0	40	2	US-09-657-276-995	Sequence 995, App
7	7	100.0	42	1	US-08-271-162-5	Sequence 5, Appli
8	7	100.0	42	1	US-08-268-348A-2	Sequence 2, Appli

9	7	100.0	42	2	US-09-623-548A-961	Sequence 961, App
10	7	100.0	42	2	US-09-623-548A-967	Sequence 967, App
11	7	100.0	42	2	US-09-623-548A-994	Sequence 994, App
12	7	100.0	42	2	US-09-657-276-961	Sequence 961, App
13	7	100.0	42	2	US-09-657-276-967	Sequence 967, App
14	7	100.0	42	2	US-09-657-276-994	Sequence 994, App
15	7	100.0	42	4	PCT-US95-08302-5	Sequence 5, Appli
16	7	100.0	42	6	5220013-12	Patent No. 5220013
17	7	100.0	42	6	5223482-12	Patent No. 5223482
18	7	100.0	43	6	5187153-12	Patent No. 5187153
19	7	100.0	55	2	US-09-823-153-10	Sequence 10, Appl
20	7	100.0	133	1	US-08-268-348A-8	Sequence 8, Appli
21	7	100.0	695	2	US-09-458-481B-4	Sequence 4, Appli
22	7	100.0	695	2	US-09-458-481B-5	Sequence 5, Appli
23	7	100.0	695	2	US-09-458-481B-6	Sequence 6, Appli
24	6	85.7	200	2	US-09-813-742A-6	Sequence 6, Appli
25	5	71.4	20	2	US-08-253-783-25	Sequence 25, Appl
26	5	71.4	20	4	PCT-US95-06726-25	Sequence 25, Appl
27	5	71.4	26	2	US-09-302-812-21	Sequence 21, Appl
28	5	71.4	26	2	US-09-511-477-21	Sequence 21, Appl
29	5	71.4	26	2	US-09-511-507-21	Sequence 21, Appl
30	5	71.4	26	2	US-09-973-451-21	Sequence 21, Appl
31	5	71.4	140	2	US-09-270-767-37585	Sequence 37585, A
32	5	71.4	140	2	US-09-270-767-52802	Sequence 52802, A
33	5	71.4	143	1	US-07-956-700B-43	Sequence 43, Appl
34	5	71.4	143	1	US-08-476-537-43	Sequence 43, Appl
35	5	71.4	143	1	US-08-485-607-43	Sequence 43, Appl
36	5	71.4	143	1	US-08-475-879-43	Sequence 43, Appl
37	5	71.4	143	2	US-09-433-043B-43	Sequence 43, Appl
38	5	71.4	178	2	US-10-104-047-3886	Sequence 3886, Ap
39	5	71.4	222	2	US-09-252-991A-26678	Sequence 26678, A
40	5	71.4	226	2	US-09-252-991A-26834	Sequence 26834, A
41	5	71.4	259	2	US-10-104-047-3455	Sequence 3455, Ap
42	5	71.4	292	2	US-09-198-452A-738	Sequence 738, App
43	5	71.4	299	2	US-09-438-185A-698	Sequence 698, App
44	5	71.4	304	2	US-09-489-039A-11956	Sequence 11956, A
45	5	71.4	319	2	US-09-328-352-7753	Sequence 7753, Ap

ALIGNMENTS

RESULT 1
US-09-623-548A-962
; Sequence 962, Application US/09623548A
; Patent No. 6849714
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudeau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; TITLE OF INVENTION: COMPONENTS
; FILE REFERENCE: 2110

Search completed: January 6, 2006, 17:01:11
Job time : 28.875 secs

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OM protein - protein search, using sw model

Run on: January 6, 2006, 16:45:55 ; Search time 63.875 Seconds
                                            (without alignments)
                                            45.790 Million cell updates/sec

Title: US-10-528-928-4
Perfect score: 7
Sequence: 1 EVRHQKL 7

Scoring table: OLIGO
                 Gapop 60.0 , Gapext 60.0

Searched: 1867569 seqs, 417829326 residues

Word size :   0

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :   Published_Applications_AA_Main:*
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                 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
                 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
                 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
                 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

         Pred. No. is the number of results predicted by chance to have a
         score greater than or equal to the score of the result being printed,
         and is derived by analysis of the total score distribution.

                                    SUMMARIES
                    %
Result   Query
   No.   Score   Match Length DB   ID   Description
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        1   7 100.0   24 5   US-10-728-246-6   Sequence 6, Appli
        2   7 100.0   40 6   US-11-066-697-962   Sequence 962, App
        3   7 100.0   40 6   US-11-066-697-968   Sequence 968, App
        4   7 100.0   40 6   US-11-066-697-995   Sequence 995, App
        5   7 100.0   42 4   US-10-656-624-6   Sequence 6, Appli
        6   7 100.0   42 6   US-11-066-697-961   Sequence 961, App
        7   7 100.0   42 6   US-11-066-697-967   Sequence 967, App
        8   7 100.0   42 6   US-11-066-697-994   Sequence 994, App

9	7	100.0	48	5	US-10-486-265-4	Sequence 4, Appli
10	7	100.0	55	3	US-09-823-153-10	Sequence 10, Appl
11	7	100.0	55	4	US-10-713-981-10	Sequence 10, Appl
12	7	100.0	740	4	US-10-367-094-194	Sequence 194, App
13	5	71.4	20	4	US-10-732-847A-24	Sequence 24, Appl
14	5	71.4	20	4	US-10-732-847A-25	Sequence 25, Appl
15	5	71.4	26	3	US-09-973-451-21	Sequence 21, Appl
16	5	71.4	26	6	US-11-058-995-21	Sequence 21, Appl
17	5	71.4	38	3	US-09-864-761-45198	Sequence 45198, A
18	5	71.4	44	4	US-10-437-963-115742	Sequence 115742,
19	5	71.4	54	4	US-10-425-115-196777	Sequence 196777,
20	5	71.4	69	4	US-10-425-115-306905	Sequence 306905,
21	5	71.4	77	4	US-10-425-115-199646	Sequence 199646,
22	5	71.4	79	3	US-09-764-878-149	Sequence 149, App
23	5	71.4	79	4	US-10-079-854-149	Sequence 149, App
24	5	71.4	85	4	US-10-424-599-191900	Sequence 191900,
25	5	71.4	87	4	US-10-437-963-119403	Sequence 119403,
26	5	71.4	88	4	US-10-424-599-197008	Sequence 197008,
27	5	71.4	92	4	US-10-425-115-317958	Sequence 317958,
28	5	71.4	95	4	US-10-425-115-185189	Sequence 185189,
29	5	71.4	98	4	US-10-425-115-294512	Sequence 294512,
30	5	71.4	102	4	US-10-425-115-192955	Sequence 192955,
31	5	71.4	111	4	US-10-425-115-347947	Sequence 347947,
32	5	71.4	112	4	US-10-425-115-187421	Sequence 187421,
33	5	71.4	113	3	US-09-925-300-1789	Sequence 1789, Ap
34	5	71.4	114	4	US-10-425-115-330643	Sequence 330643,
35	5	71.4	129	4	US-10-424-599-192420	Sequence 192420,
36	5	71.4	136	3	US-09-813-432-29	Sequence 29, Appl
37	5	71.4	136	4	US-10-174-364-29	Sequence 29, Appl
38	5	71.4	136	4	US-10-246-583-29	Sequence 29, Appl
39	5	71.4	136	4	US-10-689-832-29	Sequence 29, Appl
40	5	71.4	140	3	US-09-764-864-1077	Sequence 1077, Ap
41	5	71.4	145	4	US-10-437-963-187560	Sequence 187560,
42	5	71.4	148	4	US-10-424-599-239933	Sequence 239933,
43	5	71.4	152	4	US-10-424-599-185276	Sequence 185276,
44	5	71.4	152	5	US-10-450-763-39809	Sequence 39809, A
45	5	71.4	153	4	US-10-425-114-39975	Sequence 39975, A

ALIGNMENTS

RESULT 1
US-10-728-246-6
; Sequence 6, Application US/10728246
; Publication No. US20050026165A1
; GENERAL INFORMATION:
; APPLICANT: ORSER, Cindy
; APPLICANT: GROSSET, Anne
; APPLICANT: DAVIDSON, Eugene A.
; TITLE OF INVENTION: DETECTION OF CONFORMATIONALLY ALTERED PROTEINS AND PRIONS
; FILE REFERENCE: A28-011
; CURRENT APPLICATION NUMBER: US/10/728,246
; CURRENT FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: 10/161,061
; PRIOR FILING DATE: 2002-05-30
; PRIOR APPLICATION NUMBER: 60/295,456

```
Search completed: January  6, 2006, 17:05:01
Job time : 64.875 secs

                        GenCore version 5.1.6
                Copyright (c) 1993 - 2006  Compugen Ltd.


OM protein - protein search, using sw model

Run on:         January  6, 2006, 16:51:56 ; Search time 4.375 Seconds
                                            (without alignments)
                                            13.579 Million cell updates/sec


Title:          US-10-528-928-4
Perfect score:  7
Sequence:       1 EVRHQKL 7


Scoring table:  OLIGO
                Gapop 60.0 , Gapext 60.0


Searched:       61072 seqs, 8486849 residues


Word size :     0


Total number of hits satisfying chosen parameters:     61072


Minimum DB seq length: 0
Maximum DB seq length: 2000000000


Post-processing: Listing first 45 summaries


Database :      Published_Applications_AA_New:*
                1:  /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
                2:  /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
                3:  /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
                4:  /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
                5:  /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
                6:  /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
                7:  /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
                8:  /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*


        Pred. No. is the number of results predicted by chance to have a
        score greater than or equal to the score of the result being printed,
        and is derived by analysis of the total score distribution.


                            SUMMARIES
                    %
Result              Query
   No.   Score   Match Length DB  ID                      Description
-----------------------------------------------------------------------------
     1       4    57.1     19  6   US-10-923-605-5         Sequence 5, Appli
     2       4    57.1     19  6   US-10-934-818-5         Sequence 5, Appli
     3       4    57.1     40  7   US-11-016-706-36        Sequence 36, Appl
     4       4    57.1     40  7   US-11-098-674-12        Sequence 12, Appl
     5       4    57.1     42  6   US-10-923-605-1         Sequence 1, Appli
     6       4    57.1     42  6   US-10-934-818-1         Sequence 1, Appli
```

```
 7       4    57.1    42    7   US-11-016-706-37        Sequence 37, Appl
 8       4    57.1    43    6   US-10-934-818-6         Sequence 6, Appli
 9       4    57.1    43    6   US-10-250-581-1         Sequence 1, Appli
10       4    57.1    43    6   US-10-250-581-1         Sequence 1, Appli
11       4    57.1    65    6   US-10-467-657-9149      Sequence 9149, Ap
12       4    57.1    67    6   US-10-467-657-8570      Sequence 8570, Ap
13       4    57.1    77    6   US-10-467-657-3648      Sequence 3648, Ap
14       4    57.1    89    6   US-10-467-657-9016      Sequence 9016, Ap
15       4    57.1    91    7   US-11-074-176-352       Sequence 352, App
16       4    57.1    95    7   US-11-074-176-180       Sequence 180, App
17       4    57.1   119    6   US-10-467-657-2818      Sequence 2818, Ap
18       4    57.1   120    6   US-10-793-626-1518      Sequence 1518, Ap
19       4    57.1   129    6   US-10-467-657-2600      Sequence 2600, Ap
20       4    57.1   132    6   US-10-980-459-38        Sequence 38, Appl
21       4    57.1   132    6   US-10-980-459-40        Sequence 40, Appl
22       4    57.1   134    6   US-10-793-626-494       Sequence 494, App
23       4    57.1   134    6   US-10-793-626-1364      Sequence 1364, Ap
24       4    57.1   134    6   US-10-980-459-34        Sequence 34, Appl
25       4    57.1   134    7   US-11-091-643-2         Sequence 2, Appli
26       4    57.1   136    6   US-10-842-206-16        Sequence 16, Appl
27       4    57.1   136    6   US-10-842-206-18        Sequence 18, Appl
28       4    57.1   138    6   US-10-793-626-662       Sequence 662, App
29       4    57.1   138    6   US-10-842-206-10        Sequence 10, Appl
30       4    57.1   149    6   US-10-980-459-36        Sequence 36, Appl
31       4    57.1   155    6   US-10-842-206-12        Sequence 12, Appl
32       4    57.1   158    6   US-10-842-206-20        Sequence 20, Appl
33       4    57.1   158    6   US-10-980-459-4         Sequence 4, Appli
34       4    57.1   179    6   US-10-842-206-6         Sequence 6, Appli
35       4    57.1   179    6   US-10-842-206-24        Sequence 24, Appl
36       4    57.1   179    6   US-10-980-459-7         Sequence 7, Appli
37       4    57.1   179    6   US-10-980-459-10        Sequence 10, Appl
38       4    57.1   182    6   US-10-793-626-2836      Sequence 2836, Ap
39       4    57.1   183    6   US-10-793-626-2606      Sequence 2606, Ap
40       4    57.1   183    6   US-10-842-206-14        Sequence 14, Appl
41       4    57.1   185    6   US-10-842-206-8         Sequence 8, Appli
42       4    57.1   188    6   US-10-842-206-40        Sequence 40, Appl
43       4    57.1   188    6   US-10-980-459-32        Sequence 32, Appl
44       4    57.1   189    6   US-10-467-657-3184      Sequence 3184, Ap
45       4    57.1   197    6   US-10-842-206-39        Sequence 39, Appl
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ALIGNMENTS

RESULT 1
US-10-923-605-5
; Sequence 5, Application US/10923605
; Publication No. US20050249727A1
; GENERAL INFORMATION:
; APPLICANT: Schenk, Dale B.
; APPLICANT: Neuralab Limited
; TITLE OF INVENTION: Prevention and Treatment of Amyloidogenic Disease
; FILE REFERENCE: 15270J-004740US
; CURRENT APPLICATION NUMBER: US/10/923,605
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: US/09/322,289
; PRIOR FILING DATE: 1999-05-28

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Qy          2 VRHQ 5
               ||||
Db         84 VRHQ 87


RESULT 15
US-11-074-176-352
; Sequence 352, Application US/11074176
; Publication No. US20050250135A1
; GENERAL INFORMATION:
;  APPLICANT: Klaenhammer, Todd R.
;  APPLICANT:  Russell, William M.
;  APPLICANT:  Altermann, Eric
;  APPLICANT:  McAuliffe, Olivia
;  APPLICANT:  Peril, Andrea Azcarate
;  TITLE OF INVENTION: Nucleic Acid Sequences Encoding
;  TITLE OF INVENTION:  Stress-Related Proteins and Uses Therefore
;  FILE REFERENCE: 5051-694
;  CURRENT APPLICATION NUMBER: US/11/074,176
;  CURRENT FILING DATE:  2005-03-07
;  PRIOR APPLICATION NUMBER: 60/551,161
;  PRIOR FILING DATE: 2004-03-08
;  NUMBER OF SEQ ID NOS: 381
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 352
;   LENGTH: 91
;   TYPE: PRT
;   ORGANISM: Lactobacillus acidophilus
US-11-074-176-352

  Query Match              57.1%;  Score 4;  DB 7;  Length 91;
  Best Local Similarity   100.0%;  Pred. No. 63;
  Matches    4;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy          1 EVRH 4
               ||||
Db         52 EVRH 55
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Search completed: January 6, 2006, 17:05:27
Job time : 4.375 secs

OM protein - protein search, using sw model

Run on: January 6, 2006, 16:43:17 ; Search time 19.5417 Seconds
                                              (without alignments)
                                              34.466 Million cell updates/sec

Title: US-10-528-928-4
Perfect score: 7
Sequence: 1 EVRHQKL 7

Scoring table: OLIGO
                 Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size :   0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :   PIR_80:*
                 1: pir1:*
                 2: pir2:*
                 3: pir3:*
                 4: pir4:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

                              SUMMARIES

              %
Result   Query
   No.   Score Match Length DB   ID   Description
----
     1   7   100.0   33   2   S23094   beta-amyloid prote
     2   7   100.0   695   2   A27485   Alzheimer's diseas
     3   7   100.0   695   2   S00550   Alzheimer's diseas
     4   6   85.7   312   2   T23521   hypothetical prote
     5   6   85.7   513   2   T41011   hypothetical prote
     6   6   85.7   964   2   T41547   hypothetical prote
     7   6   85.7   1305   2   T18548   flax rust resistan
     8   5   71.4   85   2   B47354   ygdF protein - Sal
     9   5   71.4   90   2   AB2430   hypothetical prote
    10   5   71.4   131   2   T46455   hypothetical prote

RESULT 15
H72044
ribosomal protein S2 CP0050 [imported] - Chlamydophila pneumoniae (strains
CWL029 and AR39)
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C;Accession: H72044; E81619
R;Kalman, S.; Mitchell, W.; Marathe, R.; Lammel, C.; Fan, J.; Olinger, L.;
Grimwood, J.; Davis, R.W.; Stephens, R.S.
Nature Genet. 21, 385-389, 1999
A;Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis.
A;Reference number: A72000; MUID:99206606; PMID:10192388
A;Accession: H72044
A;Molecule type: DNA
A;Residues: 1-277 <ARN>
A;Cross-references: UNIPROT:Q9Z7K9; UNIPARC:UPI0000134EF4; GB:AE001652;
GB:AE001363; NID:g4376997; PIDN:AAD18835.1; PID:g4376999
A;Experimental source: strain CWL029
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.;
Hickey, E.K.; Peterson, J.; Utterback, T.; Berry, K.; Bass, S.; Linher, K.;
Weidman, J.; Khouri, H.; Craven, B.; Bowman, C.; Dodson, R.; Gwinn, M.; Nelson,
W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, S.L.; Eisen, J.; Fraser,
C.M.
Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae
AR39.
A;Reference number: A81500; MUID:20150255; PMID:10684935
A;Accession: E81619
A;Molecule type: DNA
A;Residues: 1-277 <REA>
A;Cross-references: UNIPARC:UPI0000134EF4; GB:AE002168; GB:AE002161;
NID:g7188982; PIDN:AAF37943.1; PID:g7188989; GSPDB:GN00122; TIGR:CP0050
A;Experimental source: strain AR39, HL cells
C;Genetics:
A;Gene: rs2; CP0050
C;Superfamily: Escherichia coli ribosomal protein S2

```
   Query Match              71.4%;  Score 5;  DB 2;  Length 277;
   Best Local Similarity   100.0%;  Pred. No. 61;
   Matches    5;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy         3 RHQKL 7
             |||||
Db        143 RHQKL 147
```

Search completed: January 6, 2006, 16:59:30
Job time : 20.5417 secs

OM protein - protein search, using sw model

Run on: January 6, 2006, 16:42:19 ; Search time 107.917 Seconds
                                             (without alignments)
                                             45.764 Million cell updates/sec

Title: US-10-528-928-4
Perfect score: 7
Sequence: 1 EVRHQKL 7

Scoring table: OLIGO
                 Gapop 60.0 , Gapext 60.0

Searched: 2166443 seqs, 705528306 residues

Word size :   0

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :   UniProt_05.80:*
                 1: uniprot_sprot:*
                 2: uniprot_trembl:*

     Pred. No. is the number of results predicted by chance to have a
     score greater than or equal to the score of the result being printed,
     and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	7	100.0	79	2	O35463_CRIGR	O35463 cricetulus
2	7	100.0	218	2	Q8BPV5_MOUSE	Q8bpv5 mus musculu
3	7	100.0	384	2	Q8BPC7_MOUSE	Q8bpc7 mus musculu
4	7	100.0	695	2	Q6GR78_MOUSE	Q6gr78 mus musculu
5	7	100.0	733	2	Q6P6Q5_RAT	Q6p6q5 rattus norv
6	7	100.0	770	1	A4_MOUSE	P12023 m amyloid b
7	7	100.0	770	1	A4_RAT	P08592 r amyloid b
8	7	100.0	770	2	Q53ZT3_MOUSE	Q53zt3 mus musculu
9	7	100.0	770	2	Q547B7_RAT	Q547b7 rattus norv
10	6	85.7	312	2	Q21373_CAEEL	Q21373 caenorhabdi
11	6	85.7	509	2	Q4V8J1_RAT	Q4v8j1 rattus norv
12	6	85.7	734	2	Q80V47_MOUSE	Q80v47 mus musculu